SEQ ID NO 1 versus human genomic sequence

MEGABLAST 1.2.3-Paracel [2001-11-20]

Query= LEX143seqid1
          (1311 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
AL121673.41.1.151163	392	e-106

>AL121673.41.1.151163
          Length = 151163

 Score = 392 bits (198), Expect = e-106
 Identities = 201/202 (99%)
 Strand = Plus / Plus

Query: 57   caggcccgagtgccaggcatggacggggacgctgctgctgggcacgtgccttctgtactg   116
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct: 17379 caggcccgagtgccaggcatggacggggacgctgctgctgggcacatgccttctgtactg   17438

Query: 117   cgcccgctccagcatgcccatctgcaccgtctccatgagccaggacttcggctggaacaa   176
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17439 cgcccgctccagcatgcccatctgcaccgtctccatgagccaggacttcggctggaacaa   17498

Query: 177   gaaggaggccggcatcgtgctcagcagcttcttctggggctactgcctgacacaggttgt   236
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 17499 gaaggaggccggcatcgtgctcagcagcttcttctggggctactgcctgacacaggttgt   17558

Query: 237   gggcggccacctcggggatcgg   258
             ||||||||||||||||||||||
Sbjct: 17559 gggcggccacctcggggatcgg   17580

Score = 335 bits (169), Expect = 4e-89
Identities = 169/169 (100%)
Strand = Plus / Plus

Query: 1143   ggcaggtgtcgtgggtgtgtgtctaggcggctacttgatggagaccacgggctcctggac
1202
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27949 ggcaggtgtcgtgggtgtgtgtctaggcggctacttgatggagaccacgggctcctggac
28008

Query: 1203   ttgcctgttcaaccttgtggccatcatcagcaacctggggctgtgcaccttcctggtgtt
1262
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 28009 ttgcctgttcaaccttgtggccatcatcagcaacctggggctgtgcaccttcctggtgtt
28068

Query: 1263   tggacaggctcagagggtggacctgagctctacccatgaggacctctag 1311
              |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 28069 tggacaggctcagagggtggacctgagctctacccatgaggacctctag 28117

Score = 281 bits (142), Expect = 5e-73
Identities = 142/142 (100%)
Strand = Plus / Plus

Query: 257   ggattggggggtgagaaggtcatcctgctgtcagcctctgcctggggctccatcacggccg
316
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18057 ggattggggggtgagaaggtcatcctgctgtcagcctctgcctggggctccatcacggccg
18116

Query: 317   tcaccccactgctcgcccacctgagcagtgcccacctggccttcatgaccttctcacgca
376
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18117 tcaccccactgctcgcccacctgagcagtgcccacctggccttcatgaccttctcacgca
18176

Query: 377   tcctcatgggcttgctccaagg 398
              ||||||||||||||||||||||
Sbjct: 18177 tcctcatgggcttgctccaagg 18198

Score = 262 bits (132), Expect = 5e-67
Identities = 132/132 (100%)
Strand = Plus / Plus

Query: 497   ggacgctgctgaccggggcggtgggctccctgctcctggaatggtacggctggcagagca
556
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 23240 ggacgctgctgaccggggcggtgggctccctgctcctggaatggtacggctggcagagca
23299

```
Query: 557    tcttctatttctccggcggcctcaccttgctttgggtgtggtacgtgtacaggtacctgc
616
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 23300  tcttctatttctccggcggcctcaccttgctttgggtgtggtacgtgtacaggtacctgc
23359


Query: 617    tgagtgaaaaag 628
               ||||||||||||
Sbjct: 23360  tgagtgaaaaag 23371



 Score =  240 bits (121), Expect = 2e-60
 Identities = 121/121 (100%)
 Strand = Plus / Plus


Query: 941    tgcagggcatgggccttggcctctccagcgtctttgctctgtgcctgggccacacctcca
1000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26222  tgcagggcatgggccttggcctctccagcgtctttgctctgtgcctgggccacacctcca
26281


Query: 1001   gcttctgtgagtctgtggtctttgcatcagcctccatcggcctccagaccttcaaccaca
1060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26282  gcttctgtgagtctgtggtctttgcatcagcctccatcggcctccagaccttcaaccaca
26341


Query: 1061   g 1061
               |
Sbjct: 26342  g 26342



 Score =  204 bits (103), Expect = 1e-49
 Identities = 103/103 (100%)
 Strand = Plus / Plus


Query: 396    aggggtttacttccctgccctgaccagcctgctgtcgcagaaggtgcgggagagtgagcg
455
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 21119  aggggtttacttccctgccctgaccagcctgctgtcgcagaaggtgcgggagagtgagcg
21178


Query: 456    agccttcacctacagcatcgtgggcgccggctcccagtttggg 498
               |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 21179  agccttcacctacagcatcgtgggcgccggctcccagtttggg 21221



 Score =  196 bits (99), Expect = 2e-47
 Identities = 99/99 (100%)
 Strand = Plus / Plus
```

Query: 725   gggcagccgtcgtctcccagctctctgcagcctgctccttcttcatcctcctctcctggc
784
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 24200 gggcagccgtcgtctcccagctctctgcagcctgctccttcttcatcctcctctcctggc
24259

Query: 785   tgcccaccttcttcgaggagaccttccccgacgccaagg 823
               |||||||||||||||||||||||||||||||||||||||
Sbjct: 24260 tgcccaccttcttcgaggagaccttccccgacgccaagg 24298

 Score = 190 bits (96), Expect = 2e-45
 Identities = 99/100 (99%)
 Strand = Plus / Plus

Query: 627   agatctcatcctggccttgggtgtcctggcccaaagccggccggtgtccaggcacagcag
686
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 23888 agatctcatcctggccttgggtgtcctggcccaaagccggccggtgtccaggcacaacag
23947

Query: 687   agtcccctggagacggctcttccggaagcctgctgtctgg 726
               ||||||||||||||||||||||||||||||||||||||||
Sbjct: 23948 agtcccctggagacggctcttccggaagcctgctgtctgg 23987

 Score = 182 bits (92), Expect = 4e-43
 Identities = 92/92 (100%)
 Strand = Plus / Plus

Query: 821   agggctggatcttcaacgtggttccttggttggtggcgattccggccagtctattcagcg
880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 24843 agggctggatcttcaacgtggttccttggttggtggcgattccggccagtctattcagcg
24902

Query: 881   ggtttctctctgatcatctcatcaatcagggt 912
               ||||||||||||||||||||||||||||||||
Sbjct: 24903 ggtttctctctgatcatctcatcaatcagggt 24934

 Score = 129 bits (65), Expect = 5e-27
 Identities = 65/65 (100%)
 Strand = Plus / Plus

Query: 1056   ccacagtggcatttctgttaacatccaggacttggccccgtcctgcgccggctttctgtt
1115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27136 ccacagtggcatttctgttaacatccaggacttggccccgtcctgcgccggctttctgtt
27195

```
Query: 1116  tggtg 1120
              |||||
Sbjct: 27196 tggtg 27200




  Score =  113 bits (57), Expect = 3e-22
  Identities = 57/57 (100%)
  Strand = Plus / Plus


Query: 1     atgcagccacccccagacgaggcccgcagggacatggccgggggacacccagtggtcc 57
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13448 atgcagccacccccagacgaggcccgcagggacatggccgggggacacccagtggtcc
13504




  Score = 73.8 bits (37), Expect = 2e-10
  Identities = 37/37 (100%)
  Strand = Plus / Plus


Query: 910   ggttacagagccatcacggtgcggaagctcatgcagg 946
             |||||||||||||||||||||||||||||||||||||
Sbjct: 25748 ggttacagagccatcacggtgcggaagctcatgcagg 25784




  Score = 67.9 bits (34), Expect = 2e-08
  Identities = 34/34 (100%)
  Strand = Plus / Plus


Query: 1117  ggtgtggccaacacagccggggccttggcaggtg 1150
             ||||||||||||||||||||||||||||||||||
Sbjct: 27319 ggtgtggccaacacagccggggccttggcaggtg 27352




  Database: Homo_sapiens.latestgp.masked.fa
    Posted date:  May 12, 2003  5:02 PM
  Number of letters in database: 200,810,911,373
  Number of sequences in database:  33,840


Lambda     K      H
   1.37    0.711   1.31


Gapped
Lambda     K      H
   1.37    0.711   1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
Number of Hits to DB: 0
length of query: 2624
length of database: 200,810,911,373
effective HSP length: 22
effective length of query: 1289
```

```
effective search space used:        0
T: 0
A: 0
X1: 0 ( 0.0 bits)
X2: 20 (39.6 bits)
S1: 12 (24.3 bits)
S2: 23 (46.1 bits)
```